

The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

Listing of The Claims:

1. (Canceled)

2. (Canceled)

3. (Canceled)

4. (Canceled)

5. (Canceled)

6. (Currently Amended)      A tissue information system, comprising:

a specimen-linked database comprising information about at least one tissue microarray - identified by an identifier wherein the tissue microarray comprises samples from a patient;

said tissue microarray comprises a plurality of sublocations, each sublocation identifiable by coordinates wherein after said user has inputted said identifier, the system displays an interface on said display of said user device, said interface providing a plurality of selectable coordinates corresponding to the coordinates on said tissue microarray, wherein selection of coordinates causes the system to display information about a tissue sample at the sublocation identified by said coordinates;

the specimen-linked database further comprises information regarding a plurality of samples of a known biological characteristic;

a database searching function allowing a user to design queries to obtain information from the specimen-linked database;

a relationship determination function allowing the user to identify relationships between a plurality of biological characteristics; and

at least one user device connectable to a network, comprising a display for displaying an interface onto which a user can input said identifier, said inputting enabling said user to access said database.

7. (Canceled)

8. (Canceled)

9. (Currently Amended) The tissue information system according to claim 68, wherein each coordinate is associated with a link for linking a user to the database.

10. (Original) The tissue information system according to claim 9, wherein when a user selects the link, an interface providing information categories is displayed, each information category associated with a link to a portion of the database comprising information relating to said information category.

11. (Currently Amended) The tissue information system according to claim 67, wherein after said user has inputted said identifier, said system displays an interface on said display of said user device which presents a representation of said tissue microarray.

12. (Original) The tissue information system according to claim 11, wherein said representation comprises images of tissues at different sublocations on said microarray.

13. (Original) The tissue information system according to claim 12, wherein each image is associated with a link for linking a user to said database.

14. (Currently Amended) The tissue information system according to claim 67, wherein after said user has inputted said identifier, said system displays an interface on said display of said user device which comprises one or more fields for inputting coordinates of a sublocation of a tissue microarray about which the user desires information.

15. (Original) The tissue information system according to claim 14, wherein after said user has inputted coordinates of a sublocation, said system displays an interface providing information categories relating to information available about a tissue sample at said sublocation.

16. (Original) The tissue information system according to claim 6, wherein the database comprises a relational database which relates the expression of a gene to a disease state.

17. (Original) The tissue information system according to claim 16, wherein said disease state is cancer.

18. (Currently Amended) The tissue information system according to claim 6, wherein said database comprises an autopsy subdatabase comprising information relating to one or more autopsy procedures.

19. (Original) The tissue information system according to claim 6, further comprising an information management system comprising search and relationship determining functions.

20. (Original) The tissue information system according to claim 6, wherein accessing the database provides information relating to one or more of diagnosis, prognosis, and likelihood of recurrence of a disease.

21. (Original) The tissue information system according to claim 19, wherein said relationship determining function links gene sequence information with clinical information about a tissue source carrying the gene.

22. (Original) The tissue information system according to claim 19, wherein said relationship determining function links gene expression information with clinical information about a tissue source expressing the gene.

23. (Original) The tissue information system according to claim 6, wherein said user device is a computer.

24. (Original) The tissue information system according to claim 6, wherein said user device is a wireless device.

25. (Original) The tissue information system according to claim 6, wherein the system comprises at least one server which comprises data storage media for maintaining the database.

26. (Original) The tissue information system according to claim 19, wherein after a user accesses the system, the system displays an interface on said display of said the user device for inputting information, said inputted information being stored in a portion of the database.

27. (Original) The tissue information system according to claim 26, wherein said inputted information comprises information relating to the expression of biological characteristics of tissues on the microarray, and in response to said inputting, said information management system identifies relationships between said expression and information relating to the sources of said tissues.

28. (Original) The tissue information system according to claim 27, wherein said information relating to the sources of said tissues comprises patient information.

29. (Previously presented) The tissue information system according to claim 27, wherein said information management system comprises a statistical program.

30. (Previously presented) The tissue information system according to claim 29, wherein said statistical program comprises non-hierarchical clustering of expression or sequence data with patient data.

31. (Original) The tissue information system according to claim 30, wherein said non-hierarchical clustering is k-means clustering.

32. (Original) The tissue information system according to claim 27, wherein expression information is obtained from tissues which have been exposed to a drug and the tissue information system, after being accessed by the user, displays an interface which provides information relating to one or more of: toxicity, efficacy, adverse effects, and half-life in a patient's circulation of the drug.

33. (Original) The tissue information system according to claim 32, wherein said information management system ranks drugs leads according to numbers or severity of adverse effects.

34. (Canceled)

35. (Original) The tissue information system according to claim 6, wherein said system stores newly inputted information in a temporary database until validation by a system operator.

36. (Original) The tissue information system according to claim 6, wherein said database comprises demographic or epidemiological data.

37. (Original) The tissue information system according to claim 6, wherein said database comprises information relating to the biological characteristics of non-human tissues.

38. (Original) The tissue information system according to claim 37, wherein said non-human tissues have been exposed to any of: drugs, antibodies, protein therapies, and gene therapies.

39. (Original) The tissue information system according to claim 6, 37, or 38, wherein said database comprises information relating to cell lines.

40. (Original) The tissue information system according to claim 6, wherein said database comprises molecular profiling data.

41. (Original) The tissue information system according to claim 30, wherein said molecular profiling data is obtained from a population of individuals.

42. (Original) The tissue information system according to claim 6, wherein said database comprises one or more subdatabases selected from the group consisting of: a sequence subdatabase, a protein structure subdatabase, a chemical formula database, an expression pattern subdatabase, a subdatabase comprising information relating to drug targets, a subdatabase comprising information relating to drug leads, a literature subdatabase, a medical history subdatabase, a demographic information subdatabase, and an autopsy subdatabase.

43. (Original) The tissue information management system according to claim 6, wherein said system further comprises data management software providing links to genomic data sources.

44. (Canceled)

45. (Original) The tissue information system according to claim 19, wherein said search function provides a Natural Language Query function for interpreting natural language inputted into an interface of the user device.

46. (Original) The system according to claim 6, wherein after a user accesses the system, the system displays a plurality of fields on an said display, said plurality of fields comprising information relating to one or more of: pathology, diagnosis, sample type, histology, treatment regimen, node status, expression of a biomolecule, medications being taken, and sites of secondary metastasis.

47. (Canceled)

48. (Canceled)

49. (Canceled)

50. (Canceled)

51. (Previously presented) A method for obtaining tissue information, comprising:  
  
providing a tissue microarray;  
  
providing an identifier which identifies said microarray;  
  
providing said user with access to said system according to claim 6 and displaying said interface onto which said user can input said identifier; and  
  
allowing said user to input said identifier, wherein the system, in response to said inputting, displays an interface on said display of said user device providing tissue information relating to said tissue microarray identified by the identifier.

52. (Canceled)

53. (Canceled)

54. (Canceled)

55. (Currently Amended) The method according to claim 51~~53~~, wherein, in response to said selection of said coordinates, said system displays an interface providing information categories, each information category associated with a link to a portion of the database comprising information relating to the information category.

56. (Original) The method according to claim 51, wherein after said user has inputted said identifier, said system displays an interface on said display of said user device which presents a representation of said tissue microarray.

57. (Original) The method according to claim 56, wherein said representation comprises images of tissues at different sublocations on said microarray.

58. (Currently Amended) The method according to claim 51~~53~~, wherein each image is associated with a link for linking a user to the database.

59. (Original) The method according to claim 51, wherein after said user has inputted said identifier, an interface is displayed on said display which comprises one or more fields for inputting coordinates of a sublocation of a tissue microarray about which the user desires information.

60. (Original) The method according to claim 59, wherein coordinates are inputted into said one or more fields, and in response to said inputting, said system displays an interface providing information categories relating to information available about a tissue sample at said sublocation.

61. (Original) The method according to claim 51, wherein the system further comprises a tissue information management system comprising search and relationship determining functions.

62. (Original) The method according to claim 60, further comprising the step of inputting information relating to one or more biological characteristics of a tissue sample on said microarray, into a new information interface displayed by said system on said display of said user device.

63. (Original) The method according to claim 62, wherein, in response to said inputting, said system provides information relating to one or more of: diagnosis, prognosis, and likelihood of recurrence of a disease.

64. (Original) The method according to claim 62, wherein said one or more biological characteristics comprises gene expression or gene sequence.

65. (Original) The method according to claim 60, wherein the relationship determining function of said tissue information system links gene expression data with information about the source of a tissue on the microarray.

66. (Previously presented) The method according to claim 61, wherein said information management system comprises a statistical program.

67. (Previously presented) The method according to claim 66, wherein said statistical program comprises non-hierarchical clustering.

68. (Original) The method according to claim 67, wherein said non-hierarchical clustering is k-means clustering.

69. (Original) The method according to claim 64, wherein expression data is obtained from tissues which have been exposed to a drug and the tissue information system displays an interface which provides information relating to one or more of: toxicity, efficacy, adverse effects, and/or half-life of the drug.

70. (Original) The method according to claim 64, wherein expression data is stored in a portion of the database comprising molecular profiling data from a population of individuals.

71. (Original) The method according to claim 60, further comprising the step of inputting a search query into an interface displayed by said system, wherein said information management system identifies records in said database related to one or more words in said query.

72. (Original) The method according to claim 71, wherein after said records are identified, links to said records are displayed by said system on an interface of said user device.



73. (Original) The method according to claim 51, wherein said identifier is provided to a user verbally, through an electronic messaging system, through a printed communication, or on said microarray.

74. (Original) The method according to claim 51, wherein said tissue microarray comprises cells from a patient with cancer and said system displays on an interface of said user device, a plurality of fields, said plurality of fields comprising information relating to one or more of: pathology, diagnosis, sample type, histology, treatment regimen, node status, expression of a biomolecule, medications being taken, and sites of secondary metastasis.

75. (Canceled)